

ICE-COVERED CHEMOSYNTHETIC ECOSYSTEMS: MINERAL AVAILABILITY AND MICROBIOLOGICAL ACCESSIBILITY (ICE-MAMBA). P. A. Lee¹, M. D. Dyar², E. C. Sklute², E. C. Tylor³, and J. A. Mikuchi³, ¹Hollings Marine Laboratory, College of Charleston, 331 Fort Johnson Rd, Charleston, SC 29412, leep@cofc.edu. ²Planetary Science Institute, 1700 East Fort Lowell, Tucson, AZ 85719. ³Dept. of Microbiology, University of Tennessee, M409 Walters Life Sciences, Knoxville, TN, 37996.

Introduction: The McMurdo Dry Valleys of Antarctica have long been considered important terrestrial analogs for the study of subsurface brines on Mars and sulfur-rich sub-ice oceans on Europa. Blood Falls, which lies in the Taylor Valley, is a hydrological feature at the terminus of the Taylor Glacier that results from the periodic discharge of a briny liquid from an aquifer beneath the glacier. The aquifer is thought to be the remnant of a cryo-concentrated fjord that has been isolated from the atmosphere and sunlight for at least 1.5 million years. The discharged brine is cold (-5 to -7°C), salty (8% salinity), ferrous (~400 µM) and rich in sulfate (50 mM) [1-2]. The vibrant red/orange color of Blood Falls (Figure 1) results from the oxidation of the ferrous iron to ferric iron as the brine comes into contact with the atmosphere.

Previous work has shown that the brine contains a viable, metabolically active chemosynthetic microbial community that couples the respiration of iron oxides to the use of reduced sulfur compounds as electron donors resulting in a system that is anoxic but not sulfidic [1, 3] in what has been described as a cryptic sulfur cycle [4]. Molecular analysis of the brine reveals the presence of a range of genes involved in the oxidation and reduction of sulfur, such as thiosulfate reductase (TSR), ATP sulfurylase (SAT), adenosine phosphosulfate reductase (AprAB), assimilatory sulfite reductase (ASR) and sulfur oxygenase/reductase (SOR). Notably, dissimilatory sulfite reductase (*dsrA*) genes that are responsible for the formation of sulfide

[1, 3] have not been detected. Isotopic measurements of sulfate, water, carbonate, and ferrous iron collectively indicate that reduced sulfate is quantitatively reoxidized to sulfate [1].

The ICE-MAMBA project is a collaborative effort consisting of three overlapping and integrated multidisciplinary elements. The first project is characterizing the brine metagenome and metatranscriptome. Second, we are studying changes in the iron mineralogy of the brine as it discharges. The third component will utilize the results of the first two efforts to develop microcosms using appropriate Blood Falls isolates and iron substrates for the determination of various molecular, mineralogical and metabolic biosignatures. These microcosm incubations allow changes in mineralogy to be related to products characterized from functional gene analysis and formation of volatile organic compounds (VOCs). The overarching objective of ICE-MAMBA is to link the findings from each component to provide a unified biosignature for extant life that is more robust than the individual biosignatures from each component.

Methods: This ongoing research uses a combination of tools to accomplish the goals stated above. The combined metagenomic and metatranscriptomic approach, using next-generation sequencing technology for metagenomic nucleic acid sequencing of archived and newly collected Blood Falls samples at UTK, supports identification of the genetic potential of resident microbes to link iron and sulfur metabolism, specifically targeting the genes and organisms involved. Changes in iron mineralogy are being assessed using x-ray diffraction as well as multi-temperature Mössbauer and VNIR spectroscopies at Mount Holyoke College and MIR-FTIR and Raman at Bruker Optics, Inc. Parallel brine/mineral incubations are monitored for headspace volatile organic compounds (VOCs) using Proton Transfer Reaction Mass Spectrometry (PTR-MS) at CofC.

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References: [1] Mikucki et al. (2009) *Science*, 324, 397-400. [2] Lyons et al. (2005) *Geoch. Cosm. Act.*, 69, 305-323. [3] Mikucki and Priscu (2007) *Appl. Environ. Microbiol.*, 73, 4029-4039. [4] Canfield et al. (2010) *Science*, 330, 1375-1378.



Figure 1. The outflow fan at Blood Falls at the terminus of the Taylor Glacier.